05 90
05 30

#5

```
RAW SEQUENCE LISTING              DATE: 06/04/2002
PATENT APPLICATION:  US/10/053,662A    TIME: 14:51:20

Input Set : A:\seqlisting.txt
Output Set: N:\CRF3\06042002\J053662A.raw
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ENTERED

```
 4 <110> APPLICANT: Alexandra Charlesworth
 5         Falvia Spirito
 6         Guerrino Meneguzzi
 7         John Baird
 8         Keith Linder
10 <120> TITLE OF INVENTION: ISOLATION OF THE LAMININ Y2 GENE IN
11         HORSES AND ITS USE IN DIAGNOSING JUNCTIONAL EPIDERMOLYSIS
12         BULLOSA
14 <130> FILE REFERENCE: p84us4
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C--> ```16 <140> CURRENT APPLICATION NUMBER: US/10/053,662A```
C--> ```16 <141> CURRENT FILING DATE: 2002-01-24```
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16 <160> NUMBER OF SEQ ID NOS: 32
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 3989
22 <212> TYPE: DNA
23 <213> ORGANISM: equine
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (198)...(3767)
29 <223> OTHER INFORMATION:
31 <400> SEQUENCE: 1
32 tgggtcctcc ttattcacag gtgagtcaca ccctgaaaca caggctctct tcctgtcagg      60
33 actgagtcag gtagaagagt cgataaaacc acctgatcaa ggaaaaggaa ggcacagcgg     120
34 agcgcagagt gagaactccc agcggcgagg cgccgggcag cgaccccctgc agcggcggac     180
35 cgcgcgccgg cctggcc atg cct gcg ctc tgg ctg agc tgc tac ctc tgc        230
36                     Met Pro Ala Leu Trp Leu Ser Cys Tyr Leu Cys
37                      1               5                  10
39 ttc tcg ctc ctc ctg ccc gca gcc cgg gcc acc tcc ggg agg gaa gtc      278
40 Phe Ser Leu Leu Leu Pro Ala Ala Arg Ala Thr Ser Gly Arg Glu Val
41          15              20                  25
43 tgt gat tgc aac ggg aag tcc agg caa tgc atc ttt gac cag gaa ctt      326
44 Cys Asp Cys Asn Gly Lys Ser Arg Gln Cys Ile Phe Asp Gln Glu Leu
45          30              35                  40
47 cac aaa cag aca gga aat gga ttc cgc tgc ctc aac tgc aat gac aac      374
48 His Lys Gln Thr Gly Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn
49      45              50                  55
51 act gat ggc atc cac tgc gag agg tgc aag gca gga ttt tac cga cag      422
52 Thr Asp Gly Ile His Cys Glu Arg Cys Lys Ala Gly Phe Tyr Arg Gln
53  60              65                  70                  75
55 aga gaa agg gac cgc tgt tta ccc tgc aat tgt aac tct aaa ggt tct      470
56 Arg Glu Arg Asp Arg Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser
57              80              85                  90
```

```
 59 ctt agc gct cga tgt gac aac tct gga cgg tgc agc tgt aag cca ggt        518
 60 Leu Ser Ala Arg Cys Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly
 61             95              100             105
 63 gtg aca gga gac agg tgt gac cga tgt ctg ccc ggc ttc cac aca ctc        566
 64 Val Thr Gly Asp Arg Cys Asp Arg Cys Leu Pro Gly Phe His Thr Leu
 65             110             115             120
 67 act gat gct ggg tgc gcc caa gac caa agg ctg cta gac tcc aag tgt        614
 68 Thr Asp Ala Gly Cys Ala Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys
 69     125                 130             135
 71 gac tgt gac cca gct ggc atc tca ggg ccc tgt gac tca ggc cgc tgt        662
 72 Asp Cys Asp Pro Ala Gly Ile Ser Gly Pro Cys Asp Ser Gly Arg Cys
 73 140                 145             150                 155
 75 gtc tgc aag ccg gct gtc act gga gag cgc tgt gat agg tgt cga cca        710
 76 Val Cys Lys Pro Ala Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Pro
 77                 160             165             170
 79 ggt tac tat cac ctg gat ggg gga aac cct cag ggc tgt acc cag tgt        758
 80 Gly Tyr Tyr His Leu Asp Gly Gly Asn Pro Gln Gly Cys Thr Gln Cys
 81             175             180             185
 83 ttt tgc tat ggg cat tcc gcc agc tgc cac agc tct ggg gac tac agt        806
 84 Phe Cys Tyr Gly His Ser Ala Ser Cys His Ser Ser Gly Asp Tyr Ser
 85             190             195             200
 87 gtc cat aaa atc atc tct gcc ttc cat caa gat gtt gat ggc tgg aag        854
 88 Val His Lys Ile Ile Ser Ala Phe His Gln Asp Val Asp Gly Trp Lys
 89     205                 210             215
 91 gct gtc caa aga aac ggg tct cct gca aag ctc cag tgg tca cag cgc        902
 92 Ala Val Gln Arg Asn Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg
 93 220                 225             230                 235
 95 cat cgg gat ata ttt agc tca gca cga cga tca gac cct gtc tat ttt        950
 96 His Arg Asp Ile Phe Ser Ser Ala Arg Arg Ser Asp Pro Val Tyr Phe
 97                 240             245             250
 99 gta gct cct gcc aaa ttt ctt ggg aat caa cag gtg agc tac ggg caa        998
100 Val Ala Pro Ala Lys Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln
101             255             260             265
103 agc cta tct ttt gac tac cgt gtg gat agg gga ggc aga cac cca tct       1046
104 Ser Leu Ser Phe Asp Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser
105             270             275             280
107 gcc cat gac gtg atc ctg gaa ggt gct ggt cta cgg atc aca gct ccc       1094
108 Ala His Asp Val Ile Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro
109     285                 290             295
111 ttg atg cca ctt agc aag aca ctg cct tgt ggg atc acc aag act tac       1142
112 Leu Met Pro Leu Ser Lys Thr Leu Pro Cys Gly Ile Thr Lys Thr Tyr
113 300                 305             310                 315
115 aca ttc aga tta aat gaa cat cca agc agt aat tgg agc ccc cag cta       1190
116 Thr Phe Arg Leu Asn Glu His Pro Ser Ser Asn Trp Ser Pro Gln Leu
117             320             325             330
119 agt tac ttt gag tat cgg agg tta ctg cgg aac ctc aca gcc ctg cgg       1238
120 Ser Tyr Phe Glu Tyr Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg
121             335             340             345
123 atc cga gct acc tac gga gaa tac agt act ggg tac att gac aac gtg       1286
```

```
124 Ile Arg Ala Thr Tyr Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val
125         350             355             360
127 acc ttg att tca gcc cgc ccc gtt tct gga gcc cca gcg ccc tgg gtt   1334
128 Thr Leu Ile Ser Ala Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val
129     365             370             375
131 gaa caa tgt gta tgc cct gtt ggc tac aag ggg cag ttc tgc cag gat   1382
132 Glu Gln Cys Val Cys Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp
133 380             385             390                 395
135 tgt gct tcc ggc tac aaa aga gat tca gcc aga ctg gga cct ttt ggc   1430
136 Cys Ala Ser Gly Tyr Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly
137             400             405             410
139 acc tgt att cca tgt aac tgc caa ggg gga ggg gcc tgc gat cca gac   1478
140 Thr Cys Ile Pro Cys Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp
141             415             420             425
143 aca gga gac tgt tac tca ggg gat gag aac cct gac atc cct gag tgt   1526
144 Thr Gly Asp Cys Tyr Ser Gly Asp Glu Asn Pro Asp Ile Pro Glu Cys
145         430             435             440
147 gct gac tgc ccc att ggt ttc tac aac gat cca caa gac ccc cgc agc   1574
148 Ala Asp Cys Pro Ile Gly Phe Tyr Asn Asp Pro Gln Asp Pro Arg Ser
149     445             450             455
151 tgc aag ccg tgc ccc tgt cgc aat ggg ttc agc tgc tcc gtg atg cct   1622
152 Cys Lys Pro Cys Pro Cys Arg Asn Gly Phe Ser Cys Ser Val Met Pro
153 460             465             470             475
155 gag aca gag gag gtg gtg tgc aat aac tgc ccc cag ggt gtc act ggt   1670
156 Glu Thr Glu Glu Val Val Cys Asn Asn Cys Pro Gln Gly Val Thr Gly
157             480             485             490
159 gcc cgc tgt gag ctc tgt gct gat ggc tat ttt ggg gac ccc ttc ggg   1718
160 Ala Arg Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly
161             495             500             505
163 gaa cgt ggc cca gtg agg cct tgt cag ccc tgt cag tgc aac aac aac   1766
164 Glu Arg Gly Pro Val Arg Pro Cys Gln Pro Cys Gln Cys Asn Asn Asn
165             510             515             520
167 gtg gac cct agt gcc tcc ggg aac tgt gac cgc ctg aca ggc agg tgt   1814
168 Val Asp Pro Ser Ala Ser Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys
169     525             530             535
171 ctg aag tgc atc cac aac aca gct ggg gtc cac tgt gac cag tgc aaa   1862
172 Leu Lys Cys Ile His Asn Thr Ala Gly Val His Cys Asp Gln Cys Lys
173 540             545             550                 555
175 gca ggc tac tat ggg gac ccg ttg gct ccc aat cca gca gac aag tgt   1910
176 Ala Gly Tyr Tyr Gly Asp Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys
177             560             565             570
179 cga gct tgc aac tgc aac cca gtg ggc tcg gag cct gtg gag tgt cga   1958
180 Arg Ala Cys Asn Cys Asn Pro Val Gly Ser Glu Pro Val Glu Cys Arg
181             575             580             585
183 agt gat ggc agc tgt gtt tgc aag cca ggc ttt ggt ggc ctc agc tgt   2006
184 Ser Asp Gly Ser Cys Val Cys Lys Pro Gly Phe Gly Gly Leu Ser Cys
185         590             595             600
187 gag cat gcg gca ctg acc agc tgt cca gct tgc tat aat caa gtg aag   2054
188 Glu His Ala Ala Leu Thr Ser Cys Pro Ala Cys Tyr Asn Gln Val Lys
```

```
189       605                    610                   615
191 gtt cag atg gat cag ttt atg cag cag ctc cag atc ctg gag gcc ctg    2102
192 Val Gln Met Asp Gln Phe Met Gln Gln Leu Gln Ile Leu Glu Ala Leu
193 620              625              630                   635
195 att tcg aag gct cag ggt gga gca gta ccc aac gca gag ctg gaa ggc    2150
196 Ile Ser Lys Ala Gln Gly Gly Ala Val Pro Asn Ala Glu Leu Glu Gly
197              640              645              650
199 agg atg cag cag gct gag cag gcc ctt cgg gac att ctg aga gaa gcc    2198
200 Arg Met Gln Gln Ala Glu Gln Ala Leu Arg Asp Ile Leu Arg Glu Ala
201              655              660              665
203 cag att tca caa gat gct gtt aga tcc ttc aat ctc cgg gtg gcc aag    2246
204 Gln Ile Ser Gln Asp Ala Val Arg Ser Phe Asn Leu Arg Val Ala Lys
205              670              675              680
207 gca agg act caa gag aat agc tac cgg gac cgc ctg gat gac ctc aag    2294
208 Ala Arg Thr Gln Glu Asn Ser Tyr Arg Asp Arg Leu Asp Asp Leu Lys
209      685              690              695
211 atg act gtg gaa aga gtt cgg gcc ctg ggc agt cag tat cag aac caa    2342
212 Met Thr Val Glu Arg Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Gln
213 700              705              710                   715
215 gtt cag gat act cgc agg ctc atc act cag atg cgc ctg agc ctg gag    2390
216 Val Gln Asp Thr Arg Arg Leu Ile Thr Gln Met Arg Leu Ser Leu Glu
217              720              725              730
219 gaa agt gag gct tcc ctg caa aac acc aac att cct cct tca gag cac    2438
220 Glu Ser Glu Ala Ser Leu Gln Asn Thr Asn Ile Pro Pro Ser Glu His
221              735              740              745
223 tac gtg ggg cca aat ggc ttt aaa agt ctg gct cag gag gcc acg aga    2486
224 Tyr Val Gly Pro Asn Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg
225              750              755              760
227 ttg gca gac agc cat gtt cag tca gcc agt aac atg gag caa ctg gca    2534
228 Leu Ala Asp Ser His Val Gln Ser Ala Ser Asn Met Glu Gln Leu Ala
229      765              770              775
231 aag gaa acc cag gag tat tcc aaa gag ctg atg tca ctg gtg cgc gag    2582
232 Lys Glu Thr Gln Glu Tyr Ser Lys Glu Leu Met Ser Leu Val Arg Glu
233 780              785              790                   795
235 gct ctg cag gaa gga ggc gga agc ggc agc ctg gac gga gcc gtg gtg    2630
236 Ala Leu Gln Glu Gly Gly Gly Ser Gly Ser Leu Asp Gly Ala Val Val
237              800              805              810
239 caa agg ctt gtg gga aaa ttg cag aaa act aaa tct ctg gcc cag gag    2678
240 Gln Arg Leu Val Gly Lys Leu Gln Lys Thr Lys Ser Leu Ala Gln Glu
241              815              820              825
243 ttg tcg agg gag gcc acg caa acc gac atg gaa gca gat agg tct tat    2726
244 Leu Ser Arg Glu Ala Thr Gln Thr Asp Met Glu Ala Asp Arg Ser Tyr
245              830              835              840
247 cag cat agt ctc cac ctt ctc aat tcc gtg tct cag att cag gga gtc    2774
248 Gln His Ser Leu His Leu Leu Asn Ser Val Ser Gln Ile Gln Gly Val
249      845              850              855
251 aat gat cag tcc ttg cag gta gaa gcg aag agg ctc aga caa aaa gct    2822
252 Asn Asp Gln Ser Leu Gln Val Glu Ala Lys Arg Leu Arg Gln Lys Ala
253 860              865              870              875
```

```
255 gat tct ctc tca aac cgt gtg act aag cat atg gat gag ttc aag cac     2870
256 Asp Ser Leu Ser Asn Arg Val Thr Lys His Met Asp Glu Phe Lys His
257             880                 885                 890
259 gtg caa agc aat ctg gga aac tgg gaa gaa gaa acc cgg cag ctc tta     2918
260 Val Gln Ser Asn Leu Gly Asn Trp Glu Glu Glu Thr Arg Gln Leu Leu
261             895                 900                 905
263 cag aat gga aag aat ggg aga cag aca tca gat cag ctg ctt tcc cgt     2966
264 Gln Asn Gly Lys Asn Gly Arg Gln Thr Ser Asp Gln Leu Leu Ser Arg
265             910                 915                 920
267 gcc aac ctt gct aaa agc aga gcc caa gaa gca cta agt atg ggc aat     3014
268 Ala Asn Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn
269     925                 930                 935
271 gcc act ttt tat gaa gtt gag aac atc tta aag aat ctc aga gag ttt     3062
272 Ala Thr Phe Tyr Glu Val Glu Asn Ile Leu Lys Asn Leu Arg Glu Phe
273 940                 945                 950                 955
275 gac ctg cag gtt gga gat aaa aga gca gaa gct gaa gag gcc atg aag     3110
276 Asp Leu Gln Val Gly Asp Lys Arg Ala Glu Ala Glu Glu Ala Met Lys
277             960                 965                 970
279 aga ctc tcc tac atc agc cag aag gtt gca ggt gcc agt gac aag acg     3158
280 Arg Leu Ser Tyr Ile Ser Gln Lys Val Ala Gly Ala Ser Asp Lys Thr
281             975                 980                 985
283 aag caa gca gaa gca gcc ctg ggc agt gct gct gcc gac gcc cag agg     3206
284 Lys Gln Ala Glu Ala Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg
285         990                 995                 1000
287 gca aag aat gca gcc agg gag gcc ctg gag atc tct ggc aag ata gaa     3254
288 Ala Lys Asn Ala Ala Arg Glu Ala Leu Glu Ile Ser Gly Lys Ile Glu
289     1005                1010                1015
291 cag gag ata gga ggt ctg aac ttg gaa gcc aat gtg aca gca gat gga     3302
292 Gln Glu Ile Gly Gly Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
293 1020                1025                1030                1035
295 gcc ttg gcc atg gag aag gga ctg gcc act ctg aaa agt gag atg aga     3350
296 Ala Leu Ala Met Glu Lys Gly Leu Ala Thr Leu Lys Ser Glu Met Arg
297             1040                1045                1050
299 gaa gtg gaa gga gag ctg tca agg aag gag cag gag ttt gac atg gat     3398
300 Glu Val Glu Gly Glu Leu Ser Arg Lys Glu Gln Glu Phe Asp Met Asp
301             1055                1060                1065
303 atg gac gca gtg cag atg gta att gca gag gcc caa aga gtt gaa aac     3446
304 Met Asp Ala Val Gln Met Val Ile Ala Glu Ala Gln Arg Val Glu Asn
305         1070                1075                1080
307 aga gcc aag aat gct gga gtt acg atc caa gac aca ctc aac aca ttg     3494
308 Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu
309     1085                1090                1095
311 gat ggc atc cta cac cta ata gac cag cct ggc agt gtg gat gaa gag     3542
312 Asp Gly Ile Leu His Leu Ile Asp Gln Pro Gly Ser Val Asp Glu Glu
313 1100                1105                1110                1115
315 agg ctg atc tta ctg gag cag aag ctt ttc cga gcc aag act cag atc     3590
316 Arg Leu Ile Leu Leu Glu Gln Lys Leu Phe Arg Ala Lys Thr Gln Ile
317             1120                1125                1130
319 aac agc cag cta cgg ccc ttg atg tca gag ctg gaa gag agg gca cat     3638
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VERIFICATION SUMMARY   DATE: 06/04/2002
PATENT APPLICATION: US/10/053,662A   TIME: 14:51:21

        Input Set : A:\seqlisting.txt
        Output Set: N:\CRF3\06042002\J053662A.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date